

Fig. S1

A

<u>MKTEEGKLV</u>	<u>WINGDKGYNG</u>	<u>LAEVGKKFEK</u>	<u>DTGIKVTVEH</u>	<u>PDKLEKFPQ</u>	<u>VAATGDGPDI</u>	60
<u>IFWAHDRFGG</u>	<u>YAQSGLLAEI</u>	<u>TPDKAFQDKL</u>	<u>YPFTWDVARY</u>	<u>NGKLIAYPIA</u>	<u>VEALSLLYNK</u>	120
<u>DLLPNPRTIW</u>	<u>EEIPALDKEL</u>	<u>KAKGKSALMF</u>	<u>NLQEPYFTWP</u>	<u>LIAADGGYAF</u>	<u>KYENGKYDIK</u>	180
<u>DVGVDNAGAK</u>	<u>AGLTFLLVDLI</u>	<u>KNKHMNADTD</u>	<u>YSTAEAAAFNK</u>	<u>GETAMTINGP</u>	<u>WAWSNIDTSK</u>	240
<u>VNYGVTVLPT</u>	<u>FKGQPSKPFV</u>	<u>GVLSAGINAA</u>	<u>SPNKELAKEF</u>	<u>LENYLLTDEG</u>	<u>LEAVNKDKPL</u>	300
<u>GAVALKSYEE</u>	<u>ELAKDPRIAA</u>	<u>TMENAKGGEI</u>	<u>MPNIPQMSAF</u>	<u>WYAVRTAVIN</u>	<u>AASGRQTVDE</u>	360
<u>ALKDAQTNSS</u>	<u>SNNNNNNNNN</u>	<u>NLGIEGRISE</u>	<u>FGSTSRVDCG</u>	<u>GLTGLNSGLT</u>	<u>TNPGVSAWQV</u>	420
<u>NTAYTAGQLV</u>	<u>TYNGKTYKCL</u>	<u>QPHTSLAGWE</u>	<u>PSNVPALWQL</u>	<u>Q</u>		461

B

Peptide position	[M+H] ⁺		Mass accuracy ppm	Sequence
	calculated mass	measured mass		
1-2	278.15	278.14	36	MK
3-7	563.27	563.26	18	TEEGK
8-16	1057.60	1057.60	0	LVIWINGDK
8-26	2046.10	2046.23	64	LVIWINGDKGYNGLAEVGK
27-35	1065.59	1065.59	0	KFEKDTGIK
28-30	423.22	423.21	24	FEK
36-47	1423.74	1422.73	709	VTVHEHPDKLEEK
90-99	1267.65	1267.60	39	LYPFTWDVAVR
129-138	1201.61	1201.60	8	TWEEIPALDK
129-141	1571.83	1571.82	6	TWEEIPALDKELK
191-201	1189.72	1189.71	8	AGLTFLLVDLIK
172-180	1129.55	1129.57	18	YENGKYDIK
253-274	2139.16	2139.08	37	GQPSKPFVGVLSAGINAASPDK
279-296	2097.04	2096.99	24	EFLNLYLLTDEGLEAVNK
297-306	1011.62	1011.57	49	DKPLGAVALK
307-317	1336.64	1336.63	7	SYEEELAKDPR
328-345	2110.03	2110.01	9	GEIMPNIPOMSAFWYAVR
346-355	959.53	959.52	10	TAVINAASGR
356-387	3459.57	3458.61	277	QTVDEALKDAQTNSSNNNNNNNNNLGIEGR
364-387	2575.11	2575.41	116	DAQTNSSNNNNNNNNNNNLGIEGR
388-396	983.48	983.55	71	ISEFGSTSR
397-435	3985.92 ^a	3985.88	10	VDCGGLTGLNSGLTTNPGVSAWQVNTAYTAGQLVTYNG
397-438	4378.13 ^a	4378.21	18	VDCGGLTGLNSGLTTNPGVSAWQVNTAYTAGQLVTYNGKTYK
439-461	2633.28 ^a	2633.14	53	CLQPHTSLAGWEPNSVNPALWQLQ

Fig. S1. Assignment of MALDI Peptide Mass Map to the MC ligation product (Fig. 6A).

A. Sequences detected by MALDI analysis of the MC product are underlined. Twenty-five tryptic peptide masses were assigned to the amino acid sequence of the MC protein, corresponding to sequence coverage of 49%. Amino acids matching the C-tag protein are in italic. The double underlined peptide (ISEFGSTSR - amino acids 388–396) contains the BIL splice site between amino acids Ser393 and Thr394.

B. Measured and calculated masses for tryptic peptides which identify the 50.6 kD MC protein.

^a mass corresponds to peptide with an alkylated cysteine

Fig. S2

A

<u>MKTEEGKLVI</u>	<u>WINGDKGYNG</u>	<u>LAEVGKKFEK</u>	<u>DTGIKVTVEH</u>	<u>PKLEEKFPQ</u>	<u>VAATGDGPD</u>	60
<u>IFWAHDRFGG</u>	<u>YAQSGLLAEI</u>	<u>TPDKAFQDKL</u>	<u>YPTWDVARY</u>	<u>NGKLIAYPIA</u>	<u>VEALSIIYNK</u>	120
<u>DLLPNPPTW</u>	<u>EEIPALDKEL</u>	<u>KAKGKSALMF</u>	<u>NLOPFYFTWP</u>	<u>LIAADGGYAF</u>	<u>KYENGKYDIK</u>	180
<u>DVGVDNAGAK</u>	<u>AGLTFLVDLI</u>	<u>KNKHMNADTD</u>	<u>YSIAEAAFNK</u>	<u>GETAMTINGP</u>	<u>WAMSNIDTSK</u>	240
<u>VNYGVTVLPT</u>	<u>FKGQPSKPFV</u>	<u>GVLSAGINAA</u>	<u>SPNKELAKEF</u>	<u>LENYLLTDEG</u>	<u>LEAVNKDKPL</u>	300
<u>GAVALKSYEE</u>	<u>ELAKDPRIAA</u>	<u>TMENAQKGEI</u>	<u>MPNIPQMSAF</u>	<u>WYAVRTAVIN</u>	<u>AASGRQTVDE</u>	360
<u>ALKDAQTNSS</u>	<u>SNNNNNNNN</u>	<u>NLGIEGRISE</u>	<u>FGScfaagtm</u>	<u>vstpdgerai</u>	<u>dtlkvgdiw</u>	420
<u>skpeggkpf</u>	<u>aaailathir</u>	<u>tdqpiyrlkl</u>	<u>kgkgenggae</u>	<u>desllvtbpg</u>	<u>pfyvpaghgf</u>	480
<u>vpvidlkkpgd</u>	<u>rlslsladgas</u>	<u>entssevesl</u>	<u>elylpvgkty</u>	<u>nltdvdqhtf</u>	<u>yvgklktwvh</u>	540
n						541

B

Peptide position	[M+H] ⁺		Mass	
	calculated mass	measured mass	accuracy ppm	Sequence
535-541	897.4947	897.47	27.5	LKTWVHN
537-541	656.3156	56.25	99.9	TWVHN

Fig. S2. MALDI peptide mapping of the 59.3 kD MB protein (Fig. 6A).

A. Underlined sequences correspond to peptides detected by MALDI. Uppercase letters match amino acids of the M-tag and lowercase letters match those of the BIL domain. Note that the C-terminus of the protein, Asn 541, is the penultimate C-terminal residue of the BIL sequence (Fig. 4).

B. Measured and calculated molecular masses of the two C-terminal peptides.